



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Conti-Fine, B.M.
- (ii) TITLE OF INVENTION: PREVENTION OF EXPERIMENTAL MYASTHANIA GRAVIS  
BY NASAL ADMINISTRATION OF SYNTHETIC T EPITOPE SEQUENCES
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
  - (B) STREET: 121 South Eighth Street, 1600 TCF Tower
  - (C) CITY: Minneapolis
  - (D) STATE: MN
  - (E) COUNTRY: USA
  - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: Windows 95
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/991,143
  - (B) FILING DATE: 16-DEC-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Embretson, Janet E
  - (B) REGISTRATION NUMBER: 39,665
  - (C) REFERENCE/DOCKET NUMBER: 600.423US1
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 612-373-6959
  - (B) TELEFAX: 612-339-3061
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1667 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

185 F2

AAGCACAGGC CACCACTCTG CCCTGGTCCA CACAAGCTCC GGTAGCCCAT GGAGCCCTGG 60  
CCTCTCCTCC TGCTCTTTAG CCTTTGCTCA GCTGGCCTCG TCCTGGGCTC CGAACATGAG 120  
ACCCGTCTGG TGGCAAAGCT ATTTAAAGAC TACAGCAGCG TGGTGCGGCC AGTGAAGAC 180  
CACCGCCAGG TCGTGGAGGT CACCGTGGGC CTGCAGCTGA TACAGCTCAT CAATGTGGAT 240  
GAAGTAAATC AGATCGTGAC AACCAATGTG CGTCTGAAAC AGCAATGGGT GGATTACAAC 300  
CTAAAATGGA ATCCAGATGA CTATGGCGGT GTGAAAAAAA TTCACATTCC TTCAGAAAAG 360  
ATCTGGCGCC CAGACCTTGT TCTCTATAAC AATGCAGATG GTGACTTTGC TATTGTCAAG 420  
TTCACCAAAG TGCTCCTGCA GTACACTGGC CACATCACGT GGACACCTCC AGCCATCTTT 480  
AAAAGCTACT GTGAGATCAT CGTCACCCAC TTTCCCTTTG ATGAACAGAA CTGCAGCATG 540  
AAGCTGGGCA CCTGGACCTA CGACGGCTCT GTCGTGGCCA TCAACCCGGA AAGCGACCAG 600  
CCAGACCTGA GCAACTTCAT GGAGAGCGGG GAGTGGGTGA TCAAGGAGTC CCGGGGCTGG 660  
AAGCACTCCG TGACCTATTC CTGCTGCCCC GACACCCCTT ACCTGGACAT CACCTACCAC 720  
TTCGTCATGC AGCGCCTGCC CCTCTACTTC ATCGTCAACG TCATCATCCC CTGCCTGCTC 780  
TTCTCCTTCT TAACTGGCCT GGTATTCTAC CTGCCCACAG ACTCAGGGGA GAAGATGACT 840  
CTGAGCATCT CTGTCTTACT GTCTTTGACT GTGTTCTTTC TGGTCATCGT GGAGCTGATC 900  
CCCTCCACGT CCAGTGCTGT GCCCTTGATT GGAAAATACA TGCTGTTCAC CATGGTGTTC 960  
GTCATTGCCT CCATCATCAT CACTGTGATC GTCATCAACA CACACCACCG CTCACCCAGC 1020  
ACCCATGTCA TGCCCAACTG GGTGCGGAAG GTTTTTATCG ACCTATCCC AAATATCATG 1080  
TTTTTCTCCA CAATGAAAAG ACCATCCAGA GAAAAGCAAG AAAAAAGAT TTTTACAGAA 1140  
GACATTGATA TCTCTGACAT TTCTGGAAAG CCAGGGCCTC CACCCATGGG CTTCCACTCT 1200  
CCCCTGATCA AACACCCCGA GGTGAAAAGT GCCATCGAGG GCATCAAGTA CATCGCAGAG 1260  
ACCATGAAGT CAGACCAGGA GTCTAACAAT GCGGCGGCAG AGTGGAAGTA CGTTGCAATG 1320  
GTGATGGACC ACATACTCCT CGGAGTCTTC ATGCTTGTTT GCATCATCGG AACCCTAGCC 1380  
GTGTTTGCAG GTCGACTCAT TGAATTAAAT CAGCAAGGAT GAGCAGAAAA TGAGCTGAGC 1440  
TTAGCTCTGC CTTGGAACCT ACCAGAGCAG AGAAGGGCAG GAGAGGAAGA TTTGTCTACT 1500  
TGCTCCACTC GCACCTTATCA AACGTGTTAT ATTCCATACT TATTATTGAT GATAAGATTT 1560  
ACCTTTATGT AAGTTTATGG CCTTGAAGTG TTTTCTATT GCTTCTCCCT TTAGTTCTGC 1620  
TGTCTCCCTG AAGAGTGAAC CCTCTTTAGT AAATGAAGT AATCACT 1667

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 457 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Pro Trp Pro Leu Leu Leu Leu Phe Ser Leu Cys Ser Ala Gly  
1 5 10 15  
Leu Val Leu Gly Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe  
20 25 30  
Lys Asp Tyr Ser Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val  
35 40 45

Val Glu Val Thr Val Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp  
 50 55 60  
 Glu Val Asn Gln Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp  
 65 70 75 80  
 Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys  
 85 90 95  
 Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu  
 100 105 110  
 Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val  
 115 120 125  
 Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe  
 130 135 140  
 Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln  
 145 150 155 160  
 Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val  
 165 170 175  
 Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu  
 180 185 190  
 Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val  
 195 200 205  
 Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His  
 210 215 220  
 Phe Val Met Gln Arg Leu Pro Leu Tyr Phe Ile Val Asn Val Ile Ile  
 225 230 235 240  
 Pro Cys Leu Leu Phe Ser Phe Leu Thr Gly Leu Val Phe Tyr Leu Pro  
 245 250 255  
 Thr Asp Ser Gly Glu Lys Met Thr Leu Ser Ile Ser Val Leu Leu Ser  
 260 265 270  
 Leu Thr Val Phe Leu Leu Val Ile Val Glu Leu Ile Pro Ser Thr Ser  
 275 280 285  
 Ser Ala Val Pro Leu Ile Gly Lys Tyr Met Leu Phe Thr Met Val Phe  
 290 295 300  
 Val Ile Ala Ser Ile Ile Ile Thr Val Ile Val Ile Asn Thr His His  
 305 310 315 320  
 Arg Ser Pro Ser Thr His Val Met Pro Asn Trp Val Arg Lys Val Phe  
 325 330 335  
 Ile Asp Thr Ile Pro Asn Ile Met Phe Phe Ser Thr Met Lys Arg Pro  
 340 345 350  
 Ser Arg Glu Lys Gln Asp Lys Lys Ile Phe Thr Glu Asp Ile Asp Ile  
 355 360 365  
 Ser Asp Ile Ser Gly Lys Pro Gly Pro Pro Pro Met Gly Phe His Ser  
 370 375 380  
 Pro Leu Ile Lys His Pro Glu Val Lys Ser Ala Ile Glu Gly Ile Lys  
 385 390 395 400  
 Tyr Ile Ala Glu Thr Met Lys Ser Asp Gln Glu Ser Asn Asn Ala Ala  
 405 410 415  
 Ala Glu Trp Lys Tyr Val Ala Met Val Met Asp His Ile Leu Leu Gly  
 420 425 430  
 Val Phe Met Leu Val Cys Ile Ile Gly Thr Leu Ala Val Phe Ala Gly  
 435 440 445  
 Arg Leu Ile Glu Leu Asn Gln Gln Gly  
 450 455

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